

APPLICATION SERIAL NUMBER

09920267

**DOES NOT COMPLY WITH THE
SEQUENCE RULES. See reasons below.**


**CRF contains errors according to STIC
Report. See attached report.**

June 19, 2002

ROUTING SHEET

APPLICATION TO BE DELIVERED TO:

O I P E


CHRISTINA CHAN
SUPERVISORY PATENT EXAMINER
TECHNOLOGY CENTER 1600

CP2-6C17

LOCA 0380

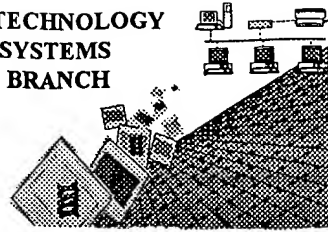
Sequence Rule Compliance Review Item

<input type="checkbox"/>	CRF, paper copy of sequence listing, and statement that both are same missing
<input checked="" type="checkbox"/>	CRF contains error(s) according to STIC Report
<input checked="" type="checkbox"/>	CRF damaged or unreadable according to STIC Report
<input type="checkbox"/>	CRF transferred from prior application is not compliant

Place an "X" in the appropriate box

RAW SEQUENCE LISTING
ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

09/920,267A

Source:

Date Processed by STIC:

600
5/16/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual- ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

09/920,267A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☒ Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ Skipped Sequences
(OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ Skipped Sequences
(NEW RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 ☐ Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 ☐ Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or Artificial Sequence
- 11 ☐ Use of <220> Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



1600

RAW SEQUENCE LISTING

DATE: 02/05/2003

PATENT APPLICATION: US/09/920,267A

TIME: 13:00:00

Input Set : A:\pto.amc

Output Set: N:\CRF4\02052003\I920267A.raw

4 <110> APPLICANT: Giles-Komar, Jill
 5 Heavner, George
 6 Snyder, Linda
 7 Trikha, Mohit
 9 <120> TITLE OF INVENTION: ANTI-DUAL INTEGRIN ANTIBODIES, COMPOSITIONS, METHODS AND
 USES
 11 <130> FILE REFERENCE: CEN0249
OK 13 <140> CURRENT APPLICATION NUMBER: US/09/920,267A
 14 <141> CURRENT FILING DATE: 2001-08-01
 16 <150> PRIOR APPLICATION NUMBER: 60/223,363
 17 <151> PRIOR FILING DATE: 2000-08-07
 19 <160> NUMBER OF SEQ ID NOS: 17
 21 <170> SOFTWARE: PatentIn Ver 3.1

ERRORED SEQUENCES

23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 5
 25 <212> TYPE: PRT
 26 <213> ORGANISM: Homo sapiens
 W--> 27 <400> SEQUENCE: 1
 29 Arg Tyr Thr Met His
 E--> 30 1 + 5 + Misaligned
 41 <210> SEQ ID NO: 3 nos. see item 3
 42 <211> LENGTH: 10 on Enr summary
 43 <212> TYPE: PRT sheet
 44 <213> ORGANISM: Homo sapiens
 W--> 45 <400> SEQUENCE: 3
 47 Glu Ala Arg Gly Ser Tyr Ala Phe Asp Ile
 E--> 48 1 + 5 10 10
 50 <210> SEQ ID NO: 4
 51 <211> LENGTH: 10 11 shown
 52 <212> TYPE: PRT
 53 <213> ORGANISM: Homo sapiens
 W--> 54 <400> SEQUENCE: 4
 56 Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala
 E--> 57 1 + 5 10 10
 59 <210> SEQ ID NO: 5
 60 <211> LENGTH: 6 7 shown
 61 <212> TYPE: PRT
 62 <213> ORGANISM: Homo sapiens
 W--> 63 <400> SEQUENCE: 5
 65 Asp Ala Ser Asn Arg Ala Thr
 1 5 fix number alignment

Does Not Comply
Corrected Diskette Needed

*same error as
 previous submission*

RAW SEQUENCE LISTING

DATE: 02/05/2003

PATENT APPLICATION: US/09/920,267A

TIME: 13:00:00

Input Set : A:\pto.amc

Output Set: N:\CRF4\02052003\I920267A.raw

E--> 66 1 5
68 <210> SEQ ID NO: 6
69 <211> LENGTH: 78
70 <212> TYPE: PRT
71 <213> ORGANISM: Homo sapiens
W--> 72 <400> SEQUENCE: 6
74 Gln Gln Arg Ser Asn Trp Pro Pro
E--> 75 1 4 5 5
364 <210> SEQ ID NO: 13
365 <211> LENGTH: 3242
366 <212> TYPE: DNA
367 <213> ORGANISM: Homo sapiens
W--> 368 <400> SEQUENCE: 13
E--> 370 ctctcctgca gggccagtca gagtggttagc agctacttag cc

3242

VERIFICATION SUMMARY

DATE: 02/05/2003

PATENT APPLICATION: US/09/920,267A

TIME: 13:00:01

Input Set : A:\pto.amc

Output Set: N:\CRF4\02052003\I920267A.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application Number
L:27 M:283 W: Missing Blank Line separator, <400> field identifier
L:30 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1 ✓
L:36 M:283 W: Missing Blank Line separator, <400> field identifier
L:45 M:283 W: Missing Blank Line separator, <400> field identifier
L:48 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3 ✓
L:54 M:283 W: Missing Blank Line separator, <400> field identifier
L:57 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4 ✓
L:57 M:252 E: No. of Seq. differs, <211> LENGTH:Input:10 Found:11 SEQ:4 ✓
L:63 M:283 W: Missing Blank Line separator, <400> field identifier
L:66 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5 ✓
L:66 M:252 E: No. of Seq. differs, <211> LENGTH:Input:6 Found:7 SEQ:5 ✓
L:72 M:283 W: Missing Blank Line separator, <400> field identifier
L:75 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6 ✓
L:75 M:252 E: No. of Seq. differs, <211> LENGTH:Input:7 Found:8 SEQ:6 ✓
L:81 M:283 W: Missing Blank Line separator, <400> field identifier
L:112 M:283 W: Missing Blank Line separator, <400> field identifier
L:139 M:283 W: Missing Blank Line separator, <400> field identifier
L:344 M:283 W: Missing Blank Line separator, <400> field identifier
L:352 M:283 W: Missing Blank Line separator, <400> field identifier
L:360 M:283 W: Missing Blank Line separator, <400> field identifier
L:368 M:283 W: Missing Blank Line separator, <400> field identifier
L:370 M:254 E: No. of Bases conflict, LENGTH:Input:32 Counted:42 SEQ:13 ✓
L:370 M:252 E: No. of Seq. differs, <211> LENGTH:Input:32 Found:42 SEQ:13 ✓
L:376 M:283 W: Missing Blank Line separator, <400> field identifier
L:384 M:283 W: Missing Blank Line separator, <400> field identifier
L:393 M:283 W: Missing Blank Line separator, <400> field identifier
L:549 M:283 W: Missing Blank Line separator, <400> field identifier